

SCORE Search Results Details for Application 10580141 and Search Result 20071214_074747_us-10-580-141-1.rng.

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This page gives you Search Results detail for the Application 10580141 and Search Result 20071214_074747_us-10-580-141-1.rng.

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MM nucleic - nucleic search, using sw model

Run on: December 14, 2007, 18:27:30 ; Search time 405 Seconds
(without alignments)
44354.964 Million cell updates/sec

Title: US-10-580-141-1
Perfect score: 1662
Sequence: 1 atgcgaataggagatcctat.....cggagaatacacatatctat 1662

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9073515 seqs, 5397694045 residues

Total number of hits satisfying chosen parameters: 18147030

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_200711:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000:*
4: geneseqn2001a:*
5: geneseqn2001b:*
6: geneseqn2002a:*
7: geneseqn2002b:*
8: geneseqn2003a:*
9: geneseqn2003b:*
10: geneseqn2003c:*
11: geneseqn2003d:*
12: geneseqn2004a:*
13: geneseqn2004b:*
14: geneseqn2004c:*
15: geneseqn2004d:*
16: geneseqn2005a:*

	42	40.2	2.4	37373	17	AEC76962	Aec76962 Bacillus
	43	40	2.4	48	2	AAZ28181	Aaz28181 Chlamydia
	44	40	2.4	48	3	AAZ99164	Aaz99164 Chlamydia
c	45	39.8	2.4	2000	8	ADA71938	Ada71938 Rice gene

ALIGNMENTS

RESULT 1

AD32410

ID AAD32410 standard; DNA; 1662 BP.

IX

XC AAD32410;

IX

DT 18-JUN-2002 (first entry)

IX

DE Chlamydia trachomatis MoPn omcB/ompB gene.

IX

W Chlamydiaceae family; chronic infection; persistent infection; pyk; nlpD;
W Cpn0585; regulatory pathway; biosynthetic pathway; ompA; ompB; hsp60;
W lipopolysaccharide; cardiovascular system; respiratory tract; therapy;
W genital tract; reproductive system; atherosclerotic tissue; macrophage;
W multiple sclerosis; conjunctiva; prophylaxis; antibacterial; gene; ds.

IX

DS Chlamydia trachomatis.

IX

TH Key Location/Qualifiers

TT CDS 1. .1662

TT /*tag= a

TT /product= "Chlamydia trachomatis MoPn omcB/ompB protein"

TT /note= "CDS does not include stop codon"

TT /partial

IX

DN WO200214516-A1.

IX

DD 21-FEB-2002.

IX

DF 17-AUG-2001; 2001WO-AU001021.

IX

DR 18-AUG-2000; 2000AU-00009540.

IX

DA (UYQU-) UNIV QUEENSLAND TECHNOLOGY.

DA (MATH/) MATHEWS S A.

IX

DI Timms P;

IX

DR WPI; 2002-269197/31.

DR P-PSDB; AAE32410.

IX

DT Detecting Chlamydial organism in its persistent phase by detecting
DT expression change of range of genes belonging to their respective
DT biosynthetic pathways when expression is compared to that of organism in
DT lytic phase.

IX

DS Disclosure; Page 156-159; 196pp; English.

IX

The invention relates to composition and methods for detecting organisms of the Chlamydiaceae family, including species of Chlamydophila and Chlamydia, in the persistent phase of their developmental cycle and for the diagnosis of chronic or persistent infections caused by such organisms. The composition is useful for modulating the expression of gene such as pyk, nlpD, Cpn0585, a gene belonging to same regulatory/biosynthetic pathway and ompA, ompB, hsp60, a gene involved in lipopolysaccharide biosynthesis. It is also useful for modulating the level and/or functional activity of an expression product of these genes, where the gene is present in an epithelial cell (selected from cardiovascular system, respiratory tract, genital tract, reproductive system or conjunctiva), macrophage, or a cell associated with atherosclerotic tissue or associated with multiple sclerosis brain tissue. The composition is useful for treatment and/or prophylaxis of a chronic infection caused by an organism of the Chlamydiaceae family in a patient. Antigen associated with the persistent phase of the developmental cycle of an organism of the Chlamydiaceae family, is useful in the manufacture of a medicament, for treating and/or preventing Chlamydiaceae infection in a patient. The present sequence is Chlamydia trachomatis MoPn omcB/ompB gene

Sequence 1662 BP; 491 A; 306 C; 384 G; 481 T; 0 U; 0 Other;

Query Match 100.0%; Score 1662; DB 6; Length 1662;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1662; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

y      1 ATGCGAATAGGAGATCCTATGAACAAACTCATCAGACGAGCTGTGACGATCTTCGCGGTG 60
      |||
b      1 ATGCGAATAGGAGATCCTATGAACAAACTCATCAGACGAGCTGTGACGATCTTCGCGGTG 60

y     61 ACTAGTGTGGCGAGTTTATTTGCTAGCGGGGTGTTAGAGACCTCTATGGCAGAGTCTCTC 120
      |||
b     61 ACTAGTGTGGCGAGTTTATTTGCTAGCGGGGTGTTAGAGACCTCTATGGCAGAGTCTCTC 120

y    121 TCTACCAACGTTATTAGCTTAGCTGACACCAAAGCGAAAGAGACCACTTCTCATCAAAAA 180
      |||
b    121 TCTACCAACGTTATTAGCTTAGCTGACACCAAAGCGAAAGAGACCACTTCTCATCAAAAA 180

y    181 GACAGAAAAGCAAGAAAAAATCATCAAAATAGGACTTCCGTAGTCCGTAAAGAGGTTACT 240
      |||
b    181 GACAGAAAAGCAAGAAAAAATCATCAAAATAGGACTTCCGTAGTCCGTAAAGAGGTTACT 240

y    241 GCAGTTCGTGATACTAAAGCTGTAGAGCCTAGACAGGATTCTTGCTTTGGCAAAATGTAT 300
      |||
b    241 GCAGTTCGTGATACTAAAGCTGTAGAGCCTAGACAGGATTCTTGCTTTGGCAAAATGTAT 300

y    301 ACAGTCAAAGTTAATGATGATCGTAATGTAGAAATCGTGCAGTCCGTTCTGAATATGCT 360
      |||
b    301 ACAGTCAAAGTTAATGATGATCGTAATGTAGAAATCGTGCAGTCCGTTCTGAATATGCT 360

y    361 ACGGTAGGATCTCCATATCCTATTGAGATTACTGCTATAGGGAAAAGAGACTGTGTTGAT 420
      |||
b    361 ACGGTAGGATCTCCATATCCTATTGAGATTACTGCTATAGGGAAAAGAGACTGTGTTGAT 420

y    421 GTAATCATTACACAGCAATTACCATGCGAAGCAGAGTTTGTAGCAGTGATCCAGCTACT 480
      |||
  
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yb 421 GTAATCATTACACAGCAATTACCATGCGAAGCAGAGTTTGTAGCAGTGATCCAGCTACT 480
 y 481 ACTCCTACTGCTGATGGTAAGCTAGTTTGGAAAATTGATCGGTTAGGACAGGGCGAAAAG 540
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 yb 481 ACTCCTACTGCTGATGGTAAGCTAGTTTGGAAAATTGATCGGTTAGGACAGGGCGAAAAG 540
 y 541 AGTAAATTACTGTATGGGTAAAACCTCTTAAAGAAGGTTGCTGCTTTACAGCTGCAACG 600
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 yb 541 AGTAAATTACTGTATGGGTAAAACCTCTTAAAGAAGGTTGCTGCTTTACAGCTGCAACG 600
 y 601 GTTTGTGCTTGTCAGAGATCCGTTTCGGTTACGAAATGTGGCCAGCCTGCTATCTGTGTT 660
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 yb 601 GTTTGTGCTTGTCAGAGATCCGTTTCGGTTACGAAATGTGGCCAGCCTGCTATCTGTGTT 660
 y 661 AAACAGGAAGGTCCAGAAAGCGCATGTTTGCGTTGCCAGTAACTTATAGAATTAATGTA 720
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 yb 661 AAACAGGAAGGTCCAGAAAGCGCATGTTTGCGTTGCCAGTAACTTATAGAATTAATGTA 720
 y 721 GTCAACCAAGGAACAGCAACAGCACGTAATGTTGTTGTGGAAAATCCTGTTCCAGATGGC 780
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 yb 721 GTCAACCAAGGAACAGCAACAGCACGTAATGTTGTTGTGGAAAATCCTGTTCCAGATGGC 780
 y 781 TATGCTCATGCATCCGGACAGCGTGTATTGACATATACTCTTGGGGATATGCAACCTGGA 840
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 yb 781 TATGCTCATGCATCCGGACAGCGTGTATTGACATATACTCTTGGGGATATGCAACCTGGA 840
 y 841 GAACAGAGAACAATCACCGTGGAGTTTTGTCCGCTTAAACGTGGTCGAGTCACAAATATT 900
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 yb 841 GAACAGAGAACAATCACCGTGGAGTTTTGTCCGCTTAAACGTGGTCGAGTCACAAATATT 900
 y 901 GCTACAGTTTCTTACTGTGGTGGACACAAAAATACTGCTAGCGTAACAACAGTGATCAAT 960
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 yb 901 GCTACAGTTTCTTACTGTGGTGGACACAAAAATACTGCTAGCGTAACAACAGTGATCAAT 960
 y 961 GAGCCTTGCGTGCAAGTTAACATCGAGGGAGCAGATTGGTCTTATGTTTGTAAGCCTGTA 1020
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 yb 961 GAGCCTTGCGTGCAAGTTAACATCGAGGGAGCAGATTGGTCTTATGTTTGTAAGCCTGTA 1020
 y 1021 GAATATGTTATCTCTGTTTCTAACCCTGGTGACTTAGTTTTACGAGACGTTGTAATTGAA 1080
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 yb 1021 GAATATGTTATCTCTGTTTCTAACCCTGGTGACTTAGTTTTACGAGACGTTGTAATTGAA 1080
 y 1081 GATACGCTTCTCCTGGAATAACTGTTGTTGAAGCAGCTGGAGCTCAGATTTCTTGTAAT 1140
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 yb 1081 GATACGCTTCTCCTGGAATAACTGTTGTTGAAGCAGCTGGAGCTCAGATTTCTTGTAAT 1140
 y 1141 AAATTGGTTTGGACTTTGAAGGAACTCAATCCTGGAGAGTCTTTACAATATAAGGTTCTA 1200
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 yb 1141 AAATTGGTTTGGACTTTGAAGGAACTCAATCCTGGAGAGTCTTTACAATATAAGGTTCTA 1200
 y 1201 GTAAGAGCTCAAACCTCCAGGGCAATTCACAAACAACGTTGTTGTGAAAAGTTGCTCTGAT 1260
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 yb 1201 GTAAGAGCTCAAACCTCCAGGGCAATTCACAAACAACGTTGTTGTGAAAAGTTGCTCTGAT 1260
 y 1261 TGCGGTATTTGTACTTCTTGCGCAGAAGCAACAACTTACTGGAAAGGAGTTGCTGCTACT 1320
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```

iy      1321 CATATGTGCGTAGTAGATACTTGTGATCCTATTTGCGTAGGAGAGAACTGTTTATCGT 1380
          |||
ob      1321 CATATGTGCGTAGTAGATACTTGTGATCCTATTTGCGTAGGAGAGAACTGTTTATCGT 1380

iy      1381 ATCTGTGTGACAAACAGAGGTTCTGCTGAAGATACAAATGTGTCCTTAATTTTGAAATTC 1440
          |||
ob      1381 ATCTGTGTGACAAACAGAGGTTCTGCTGAAGATACAAATGTGTCCTTAATTTTGAAATTC 1440

iy      1441 TCTAAAGAATTACAACCTATATCTTTCTCTGGACCAACTAAAGGAACCATTACAGGAAAC 1500
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ob      1441 TCTAAAGAATTACAACCTATATCTTTCTCTGGACCAACTAAAGGAACCATTACAGGAAAC 1500

iy      1501 ACGGTAGTGTTTGATTTCGTTACCTAGATTAGGTTCTAAAGAACTGTAGAGTTTCTGTA 1560
          |||
ob      1501 ACGGTAGTGTTTGATTTCGTTACCTAGATTAGGTTCTAAAGAACTGTAGAGTTTCTGTA 1560

iy      1561 ACGTTGAAAGCAGTATCCGCTGGAGATGCTCGTGGGGAAGCTATTCTTTCTTCCGATACA 1620
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ob      1561 ACGTTGAAAGCAGTATCCGCTGGAGATGCTCGTGGGGAAGCTATTCTTTCTTCCGATACA 1620

iy      1621 TTGACAGTTCCTGTATCTGATACGGAGAATACACATATCTAT 1662
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ob      1621 TTGACAGTTCCTGTATCTGATACGGAGAATACACATATCTAT 1662

```

RESULT 2

AEA49028

ID AEA49028 standard; DNA; 1662 BP.

IX

IC AEA49028;

IX

IT 11-AUG-2005 (first entry)

IX

IE Nucleotide sequence of 60KCRMP gene.

IX

IW 60KCRMP; cysteine-rich outer membrane protein; antibacterial; vaccine;
IW Chlamydia infection; gene; ds.

IX

IS Chlamydia muridarum.

IX

IH Key Location/Qualifiers

IT CDS 1. .1662

IT /*tag= b

IT /product= "60KCRMP"

IT sig_peptide 1. .111

IT /*tag= a

IX

IN WO2005049837-A1.

IX

ID 02-JUN-2005.

IX

IF 22-NOV-2004; 2004WO-CA002004.

IX

IR 20-NOV-2003; 2003US-0481676P.

IX

IA (AVET) AVENTIS PASTEUR LTD.

SCORE Search Results Details for Application 10580141 and Search Result 20071214_075047_us-10-580-141-2.rag.

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OM protein - protein search, using sw model

Run on: December 14, 2007, 10:25:01 ; Search time 153 Seconds
(without alignments)
2174.075 Million cell updates/sec

Title: US-10-580-141-2
Perfect score: 2882
Sequence: 1 MRIGDPMNKLIRRAVTIFAV.....ILSSDTLTVPVSDTENTHIY 554

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3405708 seqs, 601879884 residues

Total number of hits satisfying chosen parameters: 3405708

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_200711:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000:*
4: geneseqp2001:*
5: geneseqp2002:*
6: geneseqp2003a:*
7: geneseqp2003b:*
8: geneseqp2004a:*

36	138	4.8	688	4	ABB35307	Abb35307 Peptide #
37	138	4.8	688	4	AAM28810	Aam28810 Peptide #
38	138	4.8	688	4	ABG50180	Abg50180 Human liv
39	138	4.8	688	4	ABB20749	Abb20749 Protein #
40	138	4.8	688	4	AAM68511	Aam68511 Human bon
41	138	4.8	688	4	AAM16315	Aam16315 Peptide #
42	138	4.8	688	4	ABB30137	Abb30137 Peptide #
43	138	4.8	688	5	ABG38092	Abg38092 Human pep
44	138	4.8	1773	11	AEF06270	Aef06270 Human muc
45	137.5	4.8	1583	11	AES83364	Aes83364 S. agalac

ALIGNMENTS

RESULT 1

AAE20299

ID AAE20299 standard; protein; 554 AA.

XX

AC AAE20299;

XX

DT 15-JUN-2007 (revised)

DT 18-JUN-2002 (first entry)

XX

DE Chlamydia trachomatis MoPn omcB/ompB protein.

XX

KW Chlamydiaceae family; chronic infection; persistent infection; pyk; nlpD;
 KW Cpn0585; regulatory pathway; biosynthetic pathway; ompA; ompB; hsp60;
 KW lipopolysaccharide; cardiovascular system; respiratory tract; therapy;
 KW genital tract; reproductive system; atherosclerotic tissue; macrophage;
 KW multiple sclerosis; conjunctiva; prophylaxis; antibacterial; BOND_PC;
 KW 60 kDa outer membrane protein; OmcB;
 KW 60 kDa outer membrane protein [Chlamydia muridarum Nigg].

XX

DS Chlamydia trachomatis.

XX

PN WO200214516-A1.

XX

PD 21-FEB-2002.

XX

PF 17-AUG-2001; 2001WO-AU001021.

XX

PR 18-AUG-2000; 2000AU-00009540.

XX

PA (UYQU-) UNIV QUEENSLAND TECHNOLOGY.

PA (MATH/) MATHEWS S A.

XX

PI Timms P;

XX

DR WPI; 2002-269197/31.
DR N-PSDB; AAD32410.
DR PC:NCBI; gi7190756.
DR PC:SWISSPROT; Q9PJV0.

KX

PT Detecting Chlamydial organism in its persistent phase by detecting
PT expression change of range of genes belonging to their respective
PT biosynthetic pathways when expression is compared to that of organism in
PT lytic phase.

KX

PS Disclosure; Page 159-161; 196pp; English.

KX

CC The invention relates to composition and methods for detecting organisms
CC of the Chlamydiaceae family, including species of Chlamydophila and
CC Chlamydia, in the persistent phase of their developmental cycle and for
CC the diagnosis of chronic or persistent infections caused by such
CC organisms. The composition is useful for modulating the expression of
CC gene such as pyk, nlpD, Cpn0585, a gene belonging to same regulatory/
CC biosynthetic pathway and ompA, ompB, hsp60, a gene involved in
CC lipopolysaccharide biosynthesis. It is also useful for modulating the the
CC level and/or functional activity of an expression product of these genes,
CC where the gene is present in an epithelial cell (selected from
CC cardiovascular system, respiratory tract, genital tract, reproductive
CC system or conjunctiva), macrophage, or a cell associated with
CC atherosclerotic tissue or associated with multiple sclerosis brain
CC tissue. The composition is useful for treatment and/or prophylaxis of a
CC chronic infection caused by an organism of the Chlamydiaceae family in a
CC patient. Antigen associated with the persistent phase of the
CC developmental cycle of an organism of the Chlamydiaceae family, is useful
CC in the manufacture of a medicament, for treating and/or preventing
CC Chlamydiaceae infection in a patient. The present sequence is Chlamydia
CC trachomatis MoPn omcB/ompB protein

CC

CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.

KX

3Q Sequence 554 AA;

Query Match 100.0%; Score 2882; DB 5; Length 554;
Best Local Similarity 100.0%; Pred. No. 1.3e-246;
Matches 554; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2y 1 MRIGDPMNKLIRRAVTIFAVTSVASLFASGVLETSMAESLSTNVISLADTKAKETTSHQK 60
|||

2b 1 MRIGDPMNKLIRRAVTIFAVTSVASLFASGVLETSMAESLSTNVISLADTKAKETTSHQK 60

2y 61 DRKARKNHQNRTSVVRKEVTAVRDTKAVEPRQDSCFGKMYTVKVNDNRNVEIVQSVPEYA 120
|||

2b 61 DRKARKNHQNRTSVVRKEVTAVRDTKAVEPRQDSCFGKMYTVKVNDNRNVEIVQSVPEYA 120

2y 121 TVGSPYPIEITAIGKRDCVDVIITQQLPCEAEFVSSDPATTPTADGKLVWKIDRLGQGEK 180
 |||||
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 |||||
 2b 181 SKITVWVKPLKEGCCFTAATVCACPEIRSVTKCGQPAICVKQEGPESACLRCPVTYRINV 240

 2y 241 VNQGTATARNVVVENPVPDGYAHASGQRVLTYYTLGDMQPGEQRTITVEFCPLKRGRVTNI 300
 |||||
 2b 241 VNQGTATARNVVVENPVPDGYAHASGQRVLTYYTLGDMQPGEQRTITVEFCPLKRGRVTNI 300

 2y 301 ATVSYCGGHKNTASVTTVINEPCVQVNIEGADWSYVCKPVEYVISVSNPGDLVLRDVIIE 360
 |||||
 2b 301 ATVSYCGGHKNTASVTTVINEPCVQVNIEGADWSYVCKPVEYVISVSNPGDLVLRDVIIE 360

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 |||||
 2b 361 DTLSPGITVVEAAGAQISCNKLWVTLKELNPGESLQYKVLVRAQTPGQFTNNVVVKSCSD 420

 2y 421 CGICTSCAEATTYWKGVAAATHMCVVDTCDPICVGENTVYRICVTNRGSAEDTNVSLILKF 480
 |||||
 2b 421 CGICTSCAEATTYWKGVAAATHMCVVDTCDPICVGENTVYRICVTNRGSAEDTNVSLILKF 480

 2y 481 SKELQPISFSGPTKGTITGNTVVFDLPLRLGSKETVEFSVTLKAVSAGDARGEAILSSDT 540
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 2b 481 SKELQPISFSGPTKGTITGNTVVFDLPLRLGSKETVEFSVTLKAVSAGDARGEAILSSDT 540

 2y 541 LTVPVSDTENTHIY 554
 |||||
 2b 541 LTVPVSDTENTHIY 554

RESULT 2

AEA49029

ID AEA49029 standard; protein; 554 AA.

XX

AC AEA49029;

XX

DT 15-JUN-2007 (revised)

DT 11-AUG-2005 (first entry)

XX

DE Amino acid sequence of a 60KCRMP gene.

XX

KW 60KCRMP; cysteine-rich outer membrane protein; antibacterial; vaccine;

KW Chlamydia infection; BOND_PC; 60 kDa outer membrane protein; OmcB;

KW 60 kDa outer membrane protein [Chlamydia muridarum Nigg].

XX